

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/785,607C
Source: IFW/6
Date Processed by STIC: 4/7/06

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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/785,607C

DATE: 04/07/2006

TIME: 10:34:08

Input Set : A:\39780-1216R1C1D5 SAVED NOV 17 2005.TXT
 Output Set: N:\CRF4\04072006\J785607C.raw

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4 <110> APPLICANT: Ashkenazi, Avi J.
5   Fong, Sherman
6   Goddard, Audrey
7   Gurney, Austin L.
8   Napier, Mary A.
9   Tumas, Daniel
10  Wood, William I.
12 <120> TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR
13  THE TREATMENT OF DISEASES CHARACTERIZED BY A-33 RELATED
14  ANTIGENS
16 <130> FILE REFERENCE: 39780-1216R1C1D5
18 <140> CURRENT APPLICATION NUMBER: US 10/785,607C
19 <141> CURRENT FILING DATE: 2004-02-24
21 <150> PRIOR APPLICATION NUMBER: US 09/953,499
22 <151> PRIOR FILING DATE: 2001-09-14
24 <150> PRIOR APPLICATION NUMBER: US 09/254,465
25 <151> PRIOR FILING DATE: 1999-03-05
27 <150> PRIOR APPLICATION NUMBER: PCT/US98/24855
28 <151> PRIOR FILING DATE: 1998-11-20
30 <150> PRIOR APPLICATION NUMBER: PCT/US98/19437
31 <151> PRIOR FILING DATE: 1998-09-17
33 <160> NUMBER OF SEQ ID NOS: 30
35 <170> SOFTWARE: FastSEQ for Windows Version 4.0
37 <210> SEQ ID NO: 1
38 <211> LENGTH: 299
39 <212> TYPE: PRT
40 <213> ORGANISM: Homo sapiens
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46          20          25          30
47 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
48          35          40          45
49 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
50          50          55          60
51 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
52 65          70          75          80
53 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
54          85          90          95
55 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
56          100         105         110
57 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val

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58      115          120          125
59 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
60      130          135          140
61 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
62 145          150          155          160
63 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
64          165          170          175
65 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
66          180          185          190
67 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
68          195          200          205
69 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
70          210          215          220
71 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
72 225          230          235          240
73 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
74          245          250          255
75 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
76          260          265          270
77 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
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92          20          25          30
93 Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln Gly
94          35          40          45
95 Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro
96          50          55          60
97 Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala
98 65          70          75          80
99 Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val
100          85          90          95
101 Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr
102          100         105         110
103 Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp
104          115         120         125
105 Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr
106          130         135         140
107 Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg
108 145          150          155          160
109 Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile

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110 165 170 175
111 Trp Tyr Lys Gln Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr
112 180 185 190
113 Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser
114 195 200 205
115 Tyr Phe Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp
116 210 215 220
117 Ile Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys
118 225 230 235 240
119 Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser Thr
120 245 250 255
121 Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr Leu Gly
122 260 265 270
123 Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe Ala Ile Ile
124 275 280 285
125 Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr Met Ala Tyr Ile
126 290 295 300
127 Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His Val Tyr Glu Ala Ala
128 305 310 315 320
129 Arg

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135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial Sequence
138 <220> FEATURE:
139 <223> OTHER INFORMATION: Consensus DNA Sequence
141 <400> SEQUENCE: 3

142 ctctttgcaca actggatca ctttcaagtc cgtgacacgg gaagacactg ggacatacac 60
143 ttgtatggtc tctgaggaag gcggcaacag ctatggggag gtcaagggtca agtcatcg 120
144 gcttgtgcct ccatccaagc ctacagttaa catccccctcc tctgccacca ttggaaaccg 180
145 ggcagtgtcg acatgttcag aacaagatgg ttccccacct tctgaataaca cctggttcaa 240
146 agatggata gtgatgccta cgaatcccaa aagcaccgt gccttcagca actcttccta 300
147 tgtcctgaat cccacaacag gagagcttgt ctgtatccc ctgtcagccct ctgataactgg 360
148 agaatacagc tgtgagggcac ggaatggta 390

150 <210> SEQ ID NO: 4
151 <211> LENGTH: 726
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Consensus DNA Sequence
158 <400> SEQUENCE: 4

159 ttcagtcctt ctcgcgttag tcgcggagct gtgttctgtt tcccaaggagt cttcgccgg 60
160 ctgttgcgtc caggcgcc tgatcgcat gggacaaag ggcggcaagtc gagaggaaac 120
161 tttgtgcctt cttcatatttgc ggcattttgtt tttgtccctt ggcattggc agtgttacag 180
162 ttgcactctt ctgaaccttga agtcagaatt cctgagaata atcctgtgaa ttgttctgt 240
163 gcttactcggtt gctttcttc tccccgtgtt gatgtggatgtt gatgtggatgg agacaccacc 300
164 agactcggtt gctataataa caagatcaca gcttcctatg aggaccgggt gaccccttg 360
165 ccaactggta tcaccccaa gtccgtgaca cggaaagaca ctgggacata cacttgtatg 420
166 gtctctgagg aaggcggcaa cagctatggg gaggtcaagg tcaagctcat cgtgcttgc 480

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167 cctccatcca agcctacagt taacatcccc tcctctgccca ccattggaa ccgggcagtg 540
 168 ctgacatgct cagaacaaga tggttcccca ccttctgaat acacctgtt caaagatggg 600
 169 atagtatgc ctacgaatcc caaaaaggacc cgtccctca gcaactcttc ctatgtcctg 660
 170 aatcccaccaa caggagagct ggtcttgat cccotgtcag cctctgatac tggagaatac 720
 171 agctgt 726
 173 <210> SEQ ID NO: 5
 174 <211> LENGTH: 1503
 175 <212> TYPE: DNA
 176 <213> ORGANISM: Artificial Sequence
 178 <220> FEATURE:
 179 <223> OTHER INFORMATION: Consensus DNA Sequence
 181 <400> SEQUENCE: 5
 182 gcaggcaaag taccagggcc gcctgcatgt gagccacaag gttccaggag atgtatccct 60
 183 ccaattgagc accctggaga tggatgaccg gagccactac acgtgtgaag tcacctggca 120
 184 gactcctgat ggcaaccaag tcgtgagaga taagattact gagctccgtg tccagaaact 180
 185 ctctgtctcc aagcccacag tgacaactgg cagoggttat ggcttcacgg tgccccaggg 240
 186 aataggatt agcctcaat gccagggttc ggggttctcc tcccatcaat tatatttgt 300
 187 ataagcaaca gactaataac cagggAACCC atcaaagttag caaccctaag taccttactc 360
 188 ttcaagcctg cggtgatagc cgactcaggc tcctatttct gcactgc当地 gggccaggtt 420
 189 ggctctgagc agcacagcga cattgtgaag ttttggtca aagactcctc aaagctactc 480
 190 aagaccaaga ctgaggcacc tacaaccatg acataaccct tgaaagcaac atctacagt 540
 191 aagcagtccct gggactggac cactgacatg gatggctacc ttggagagac cagtgctggg 600
 192 ccagggaaaga gcctgc当地 ct当地ccatca ttc当地tggc当地 ctgtatggg 660
 193 gtttttacca tggccatata catgctctgt cggaagacat cccaaacaaga gcatgtctac 720
 194 gaagcagcca gggcacatgc cagagaggcc aacgactctg gagaaccat gagggtggcc 780
 195 atcttcgcaa gtggctgctc cagtgttag ccaactccc agaatctggg gcaacaacta 840
 196 ctctgatgag ccctgc当地 gacaggagta ccagatcatc gccc当地atca atggcaacta 900
 197 cgccccccctg ctggacacag ttccctctgg ttatgagtt ctggccactg agggcaaaag 960
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 202 ctggtaactcc tctctaaata ccagaggaa gatgccc当地 gcactaggac ttgtctcatca 1260
 203 tgccctacaga cactattcaa ttggccatc ttgccc当地 aagaccggag gggaggctca 1320
 204 gctctgccc当地 ctcagaggac cagctatatac caggatcatt tctcttctt cagggccaga 1380
 205 cagctttaa ttgaaattgt tatttcacag gccagggttc agttctgctc ctccactata 1440
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 207 aaa 1503
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 210 <211> LENGTH: 319
 211 <212> TYPE: PRT
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 214 <400> SEQUENCE: 6
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 216 1 5 10 15
 217 Val Thr Val Asp Ala Ile Ser Val Glu Thr Pro Gln Asp Val Leu Arg
 218 20 25 30
 219 Ala Ser Gln Gly Lys Ser Val Thr Leu Pro Cys Thr Tyr His Thr Ser
 220 35 40 45

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221 Thr Ser Ser Arg Glu Gly Leu Ile Gln Trp Asp Lys Leu Leu Thr
222      50          55          60
223 His Thr Glu Arg Val Val Ile Trp Pro Phe Ser Asn Lys Asn Tyr Ile
224      65          70          75          80
225 His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile Ser Asn Asn Ala Glu
226      85          90          95
227 Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu Thr Met Ala Asp Asn
228      100         105         110
229 Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser Asp Leu Glu Gly Asn
230      115         120         125
231 Thr Lys Ser Arg Val Arg Leu Leu Val Leu Val Pro Pro Ser Lys Pro
232      130         135         140
233 Glu Cys Gly Ile Glu Gly Glu Thr Ile Ile Gly Asn Asn Ile Gln Leu
234      145         150         155         160
235 Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro Gln Tyr Ser Trp Lys
236      165         170         175
237 Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro Ala Ser
238      180         185         190
239 Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser Gly Tyr
240      195         200         205
241 Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr Gln Phe Cys Asn Ile
242      210         215         220
243 Thr Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr Val Gly
244      225         230         235         240
245 Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile Ile Ile
246      245         250         255
247 Tyr Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp Lys Glu
248      260         265         270
249 Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro Pro Glu Gln Leu
250      275         280         285
251 Arg Glu Leu Ser Arg Glu Arg Glu Glu Asp Asp Tyr Arg Gln Glu
252      290         295         300
253 Glu Gln Arg Ser Thr Gly Arg Glu Ser Pro Asp His Leu Asp Gln
254      305         310         315
257 <210> SEQ ID NO: 7
258 <211> LENGTH: 2181
259 <212> TYPE: DNA
260 <213> ORGANISM: Homo sapiens
262 <400> SEQUENCE: 7
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264 tttaggcctc ttggtagca ggaggctgga agaaaggaca gaagtagctc tggctgtat 120
265 gggatctta ctgggcctgc tactcctgg gcacctaaca gtggacactt atggccgtcc 180
266 catcctggaa gtgccagaga gtgtAACAGG accttggaaa gggatgtga atttccctg 240
267 caccttatgac cccctgcaag gctacaccca agtcttggtg aagtggctgg tacaacgtgg 300
268 ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc agcaggcaaa 360
269 gtaccaggcc cgcctgcatg tgagccacaa ggttccagga gatgtatccc tccaaattgag 420
270 caccctggag atggatgacc ggagccacta cacgtgtgaa gtcacccgtc agactcctga 480
271 tggcaaccaa gtcgtgagag ataagattac tgagctccgt gtccagaaac tctctgtctc 540
272 caagcccaca gtgacaactg gcagcggtta tggcttcacg gtgccccagg gaatgaggat 600

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VERIFICATION SUMMARY

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